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# High throughput isolation and genetic analysis of prenatal samples

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## 1 TITLE

High throughput isolation and genetic analysis of prenatal samples.

## 2 FIELD OF THE INVENTION

THIS INVENTION relates to the combinations of isolation/enrichment of cells from samples, the genetic identification and analysis of such cells and the automated processing of resultant data to enable high throughput genetic analysis and thus practical application. More particularly, this invention relates to high throughput enrichment of fetal cells from cervical samples, and in particular, Pap smears. In a particular form, this invention relates to use of fetal cells enriched from cervical samples for subsequent genetic analysis such as Down syndrome, sex and single gene defects. Particular embodiments of this invention utilize cell isolation procedures such as laser micro-dissection, magnetic and/or fluorescent activated cell sorting, singly and in combination, to enrich fetal cells to levels of purity that readily enable nucleic acid isolation for genetic analysis. Particular embodiments of this invention utilize techniques such as nucleic acid amplification and/or a variety of analysis techniques such as multiplex PCR to subsequently genetically analyse pooled or single cells.

## 3 BACKGROUND OF THE INVENTION

Genetic defects are *the* major cause of embryonic, fetal and neonatal death as well as being responsible for a large proportion of childhood disabilities. The life-long cost of these disabled children to society is enormous. Although many defects are detected by the annual ~50,000

1 prenatal tests in Australia, tests are only offered to high-risk mothers as  
2 they are invasive (~1% risk of miscarriage) and/or expensive. One result of  
3 current screening strategies is that the vast majority of babies with genetic  
4 defects are born to the low-risk population. Currently prenatal diagnosis of  
5 chromosomal and single gene disorders requires the withdrawal of fetal cells  
6 from the uterine cavity by invasive procedures such as amniocentesis or  
7 chorionic villus sampling (CVS). These techniques, although highly reliable,  
8 carry procedurally related risks such as miscarriage (0.5-1%), require a  
9 high level of technical expertise, can take several weeks for results and can  
10 only be performed relatively late in pregnancy. The miscarriage risk and  
11 high cost limit availability limits the availability of prenatal diagnosis to high  
12 risk mothers only.

13 Current prenatal risk assessment has two main limitations. Firstly,  
14 high risk mothers are offered tests even though most (~95%) do not have  
15 an affected fetus, resulting in unnecessary miscarriage risk and high cost.  
16 Secondly, affected children from low risk groups are usually not identified.

17 Currently prenatal diagnosis of chromosomal and single gene  
18 disorders requires the extraction of fetal cells from the uterine cavity by  
19 invasive procedures such as amniocentesis or chorionic villus sampling  
20 (CVS). These techniques, although highly reliable, carry procedurally related  
21 risks such as miscarriage (0.5-1%), require a high level of technical  
22 expertise, take several weeks for results and can only be performed  
23 relatively late in pregnancy. Thus, they are only offered to women  
24 considered at high risk due to age, genetic history or other indicative  
25 factors.

26 One less invasive alternative approach is to use maternal blood as a  
27 source of fetal cells for which many fetal cell enrichment methods have

1        been developed, for example as described in United States Patent  
2        5,629,147, United States Patent 5,646,004 and International Publication  
3        WO 98/02528.

4                However major technical difficulties remain due to the extremely low  
5        numbers of fetal cells found in the maternal circulation, the extreme  
6        difficulties in isolating such cells, the positive identification of fetal cells and  
7        the presence of fetal cells from previous pregnancies which may confound  
8        identification and diagnosis.

9                The presence of fetal cells in the endocervical canal was first  
10       published in Shettes, 1971, Nature **230** 52. Since then there have been  
11       many studies confirming the presence of fetal cells with varying success  
12       during the first trimester (Fejgin *et al.*, 2001, Prenatal Diagnosis **21** 619;  
13       EN.REFLIST These studies all confirm that the number of fetal cells present  
14       in the endocervical canal of pregnant women is extremely low and secondly  
15       that these cells are difficult to isolate.

16               Accordingly, the value of maternal cervical samples as a source of  
17       fetal cells for genetic analysis has remained controversial. Additionally,  
18       there have been major concerns as to the invasiveness and safety of  
19       cervical sampling and the practicality of using cervical samples as a source  
20       of relatively low abundance fetal cells. Indeed, Overton *et al.*, 1996, J. Am.  
21       Obstet. Gynecol. **175** 382 concluded that fetal cells cannot be obtained  
22       from the endocervix by minimally invasive techniques in sufficient yield for  
23       prenatal genetic diagnosis.

24               More recently Cioni *et al.*, 2003 Prenatal Diagnosis **23** 168-171  
25       confirmed that fetal cells were not detected in a consistent and reliable  
26       fashion and therefore such sampling techniques cannot be regarded as a  
27       promising tool towards minimally invasive prenatal diagnosis.

1           It has been shown (Kingdom et al., 1995 Obstetrics and  
2           Gynaecology, 86 pp 283-288) that fetal cells can be isolated from cervical  
3           samples such as PAP smears using fluorescently labelled antibodies to  
4           remove maternal cells (negative enrichment) and extract fetal cells (positive  
5           enrichment) with subsequent genetic analysis in a similar manner to that  
6           performed for fetal cells in maternal blood, Immunology, 30 (2-3) pp.194-  
7           201; Durrant et al., 1996 British Journal Of Obstetrics And Gynaecology,  
8           103, (3), 219-222). However such techniques are expensive, time intensive  
9           and are limited in sample throughput to <10 samples per day, which is  
10          insufficient for the high throughput required for cost-effective clinical  
11          application. For the purposes of this invention, high throughput refers to the  
12          ability to process in excess of 50 samples per 24hr day.

13           Previous work has identified five main difficulties in applying  
14          performing genetic analysis from cervical cells at a high throughput level  
15          sufficient for practical application.

- 16
- 17          1. Obtaining sufficient cells. Attempts to obtain fetal cells from the cervix of  
18          pregnant women have been hampered by the need to retrieve the large  
19          number of cells required for genetic diagnosis. Although this requirement  
20          has been partially overcome by no longer requiring large numbers of  
21          cells due to recent advances such as multiplex fluorescent PCR which  
22          now allow multiple genetic analyses from single cells, single cell  
23          multiplex PCR remains a highly technical process practiced by very few  
24          laboratories worldwide due to its high complexity. Previous work has  
25          indicated that fetal cells are not detected in a consistent and reliable  
26          fashion and therefore cannot be regarded as a promising tool for  
27          prenatal analysis.

1           2. Isolation of fetal cells from the sample. Recent results suggest that fetal  
2           cells can be isolated and diagnosed in only ~22% of cases due to the  
3           presence of "contaminating" maternal cells. Previous approaches have  
4           generally concentrated on isolating cervical cells by morphology or cell  
5           sorting. Unfortunately, morphology grading is extremely time-  
6           consuming, expensive and generally unreliable and inaccurate. Cell  
7           sorting such as FACS or MACS has been generally unspecific resulting in  
8           either major maternal contamination and misdiagnosis or insufficient  
9           fetal cells. This remains a major limitation to practical application.

10          3. Genetic identification of cells to determine fetal source. It is essential to  
11          identify the isolated cells as being fetal to avoid misdiagnosis from  
12          maternal cells. Although single cell DNA fingerprinting techniques such  
13          as single cell multiplex PCR can be used to forensically identify the  
14          source of a single cell, again single cell multiplex PCR remains a highly  
15          technical process practiced by very few laboratories worldwide due to its  
16          high complexity. However results from fetal cells were not detected in a  
17          consistent and reliable fashion and therefore cannot be regarded as a  
18          promising tool.

19          4. Genetic diagnosis from small cell numbers. Diagnosis from single or low  
20          numbers of cells is extremely difficult. Fetal cells have been identified in  
21          cervical samples mainly by the identification of male cells within the  
22          sample, aneuploidy screening (the primary reason for prenatal diagnosis)  
23          cannot usually be performed nor diagnosis made if the fetus is female.  
24          This requirement has been partially overcome by recent advances such  
25          as multiplex fluorescent PCR which now allow multiple genetic analyses  
26          from single cells. However again results from fetal cells were not



1 detected at a consistent and reliable enough level to be considered as a  
2 promising tool towards minimally invasive prenatal diagnosis.

3 5. Sample collection. The most recent work on PAP smears have utilised so  
4 called "thick section" PAP smears. However clinical PAP smears  
5 collections are moving towards a "thin section" smears which have not  
6 previously been used for fetal cell isolation.

7  
8 Each of the five major difficulties above have singly, and particularly in  
9 combination, prevented practical application of non-invasive prenatal  
10 diagnosis.

11 However, by improving current methods and developing new methods in  
12 combination, we have invented a novel high throughput method, to rapidly  
13 and efficiently accurately target and genetically diagnose affected babies in  
14 both high-risk mothers and previously designated low risk pregnancies. For  
15 the first time non-invasive prenatal diagnosis is now a practical application  
16 and will have enormous health, social and economic benefit.

#### 18 **4 SUMMARY OF THE INVENTION**

19 Notwithstanding the prior art teaching that cervical samples are very  
20 poor sources of fetal cells for genetic analysis, the present inventors have  
21 developed a high throughput method encompassing reliable and efficient  
22 combination of methods which isolate and enrich fetal cells from cervical  
23 samples, performed genetic analysis (DNA fingerprinting and/or genetic  
24 diagnosis/screening) with subsequent data analysis which enables sufficient  
25 high-throughput processing for practical application.

1           In one aspect, the invention provides a high throughput method of  
2 cell isolation including the step of enriching one or more fetal cells from a  
3 cervical sample.

4           In another aspect, the invention provides a high throughput method  
5 of obtaining a nucleic acid sample, including the step of isolating a nucleic  
6 acid from one or more fetal cells that have been enriched from a cervical  
7 sample.

8           In yet another aspect, the invention provides a high throughput  
9 method of genetic analysis including the step of analyzing a nucleic acid  
10 obtained from one or more fetal cells that have been enriched from a  
11 cervical sample.

12           In a further aspect, the invention relates to the high throughput use  
13 of one or more fetal cells enriched from a cervical sample for genetic  
14 analysis.

15           In a further aspect, the invention combines incremental  
16 improvements over a number of steps (isolation, DNA fingerprinting and  
17 genetic analysis and data processing), which combine to give a significantly  
18 increased throughput sufficient for practical application.

19           In a further aspect, the invention comprises multiple aspects above.

20           It will also be appreciated that other analyses also contemplated by  
21 the present invention include biochemical analysis, morphological analysis,  
22 histology, cytology, cell culture and the like as well as a variety genetic  
23 analysis including nucleic acid amplification methods such as PCR, CGH  
24 (comparative genome hybridization), SNPs (single nucleotide  
25 polymorphisms), FISH (fluorescent in situ hybridization) and the like.

1           In a still further aspect, the invention relates to the high throughput  
2 use of one or more fetal cells enriched from a cervical sample for the  
3 isolation of a nucleic acid sample.

4           In a yet further aspect, the invention relates to high throughout use  
5 of a cervical sample for enrichment of one or more fetal cells for the  
6 isolation of a nucleic acid sample.

7           In a still yet further aspect, the invention relates to high throughout  
8 use of a cervical sample for enrichment of one or more fetal cells for genetic  
9 analysis.

10          The invention also relates to high throughout enrichment steps  
11 described herein to enrich fetal material from cervical samples.

12          The invention also relates to the high throughout automation of steps  
13 described herein to enrich fetal material from cervical samples.

14          The invention also relates to any combination of isolation/enrichment  
15 techniques with any combination of nucleic amplification and/or genetic  
16 identification techniques such as DNA identification, and/or genetic  
17 diagnosis and/or automated data analysis to allow sufficiently high  
18 throughput for practical application.

19          It will be appreciated by the skilled addressee that any and all of  
20 these high throughput techniques can be readily applied to a variety of  
21 samples including, but not limited to, blood, vaginal cells, PAP smears (both  
22 thin and thick specimens).

23          Preferably, a cervical sample is obtained using an endocervical brush  
24 or cytobrush.

25          More preferably, the cervical sample is a Pap smear.

26          In a preferred embodiment, the invention provides a method of fetal  
27 cell analysis including any combination of the steps of:

- 1 (i) enriching fetal cells from a Pap smear sample according to
- 2 physical characteristics such as size, morphology and/or
- 3 granularity; and/or
- 4 (ii) positively selecting fetal cells from the cells enriched in step (i)
- 5 and/or in using at least one antibody that binds a fetal
- 6 cell antigen.
- 7 (iii) Amplification of generic nucleic acid from isolated sample from
- 8 step (ii)
- 9 (iv) Genetic Identification product from step (iii) using techniques
- 10 such as DNA fingerprinting
- 11 (v) Genetic analysis of product from step (ii), (iii) and/or (iv)
- 12 including but not limited to specific genetic analysis methods
- 13 such as multiplex PCR, SNPs, CGH, FISH, RT-PCT and the like.
- 14 It will be appreciated that steps (v) and (vi) can be combined
- 15 into a single analysis procedure
- 16 (vi) Detection of products from steps (iii), (iv) and/or (v) for
- 17 example utilising nucleic acid separation technologies such as a
- 18 DNA sequencer
- 19 (vii) automated data processing to create analysis report from step
- 20 (vi)

21  
22 Throughout this specification, unless otherwise indicated, "comprise",  
23 "comprises" and "comprising" are used inclusively rather than exclusively,  
24 so that a stated integer or group of integers may include one or more other  
25 non-stated integers or groups of integers.

26

## 5 BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. Diagram of Invention Overview

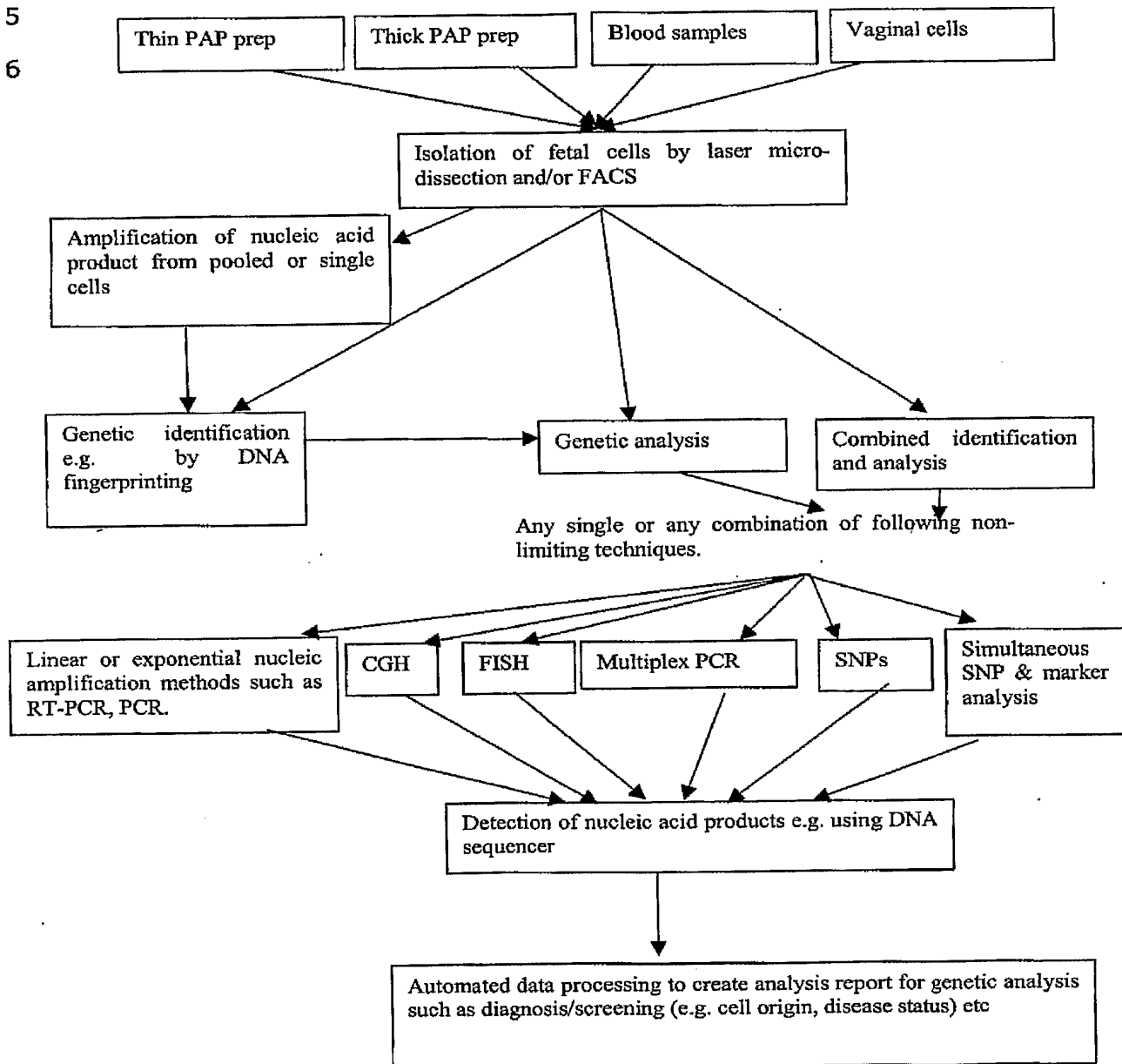


Diagram is for simplicity only and should not be construed to indicate or limit possible embodiments.

1 DETAILED DESCRIPTION OF THE INVENTION  
2

3 The present invention provides a variety of methods applicable to  
4 genetic analysis of fetal cells from maternal samples, and in particular, from  
5 cervical Pap smears. Such methods include the steps detailed previously  
6 comprising cell isolation, nucleic acid amplification, genetic identification  
7 and analysis and automated data processing.

8 It will also be appreciated that the present invention is applicable to  
9 isolation or enrichment of other cells of non-maternal origin including, but  
10 not limited to, embryonic cells, sperm cells and any cells of cytotrophoblast  
11 or syncytiotrophoblast origin.

12 It should also be appreciated that the present invention is applicable  
13 to isolation or enrichment of other cells of non-maternal origin from a  
14 variety of other sources such as maternal blood, vaginal cells and the like.

15 For the purposes of this invention, by "*isolated*" is meant material  
16 that has been removed from its natural state or otherwise been subjected  
17 to human manipulation. Isolated material may be substantially or  
18 essentially free from components that normally accompany it in its natural  
19 state, or may be manipulated so as to be in an artificial state together with  
20 components that normally accompany it in its natural state.

21 By "*enrich*", "*enriched*" and "*enrichment*" in the context of cell  
22 isolation is meant that cells are obtained in a higher frequency or proportion  
23 compared to their frequency or proportion in a starting sample prior to  
24 enrichment. In this context enrichment is also taken to include 100%  
25 enrichment where the fetal cell or cells exist in the absence of maternal  
26 cells.

27 Suitably, fetal cells are enriched from a cervical sample. Such  
28 samples include and encompass any sample obtained from the endocervix

1 inclusive of endocervical lavage, aspiration, swabbing; cytobrush samples;  
2 transcervical samples (TCCs) and Pap smears

3 Preferably, the cervical sample is a Pap smear.

4 As used herein, a Pap smear is a biological sample comprising one or  
5 more cells collected, obtained as a scraping from the cervix.

6 Typically, a metal or plastic instrument such as a speculum is placed  
7 in the vagina to allow visualization of the interior of the vagina and the  
8 cervix. A sampling instrument such as a small wooden spatula is used to  
9 scrape the outside of the cervix and thereby obtain the cervical sample.

10 For the purposes of cervical cancer screening, the scrapings are  
11 placed on a glass slide and used for microscopic examination to detect  
12 changes in the cells of the cervix. Pap smears are a routine and safe  
13 screening procedure to find early warning signs of cervical cancer. The  
14 present invention provides a new use of Pap smears as a source of fetal  
15 cells for enrichment and subsequent analysis.

16 In the context of the present invention, said one or more cells  
17 typically comprises maternal cells and fetal cells.

18 For the particular purpose of fetal cell isolation, it is preferred that  
19 the Pap smear is obtained at between 5 and 31 weeks gestation.

20 Cell enrichment may be performed by one or more high throughput  
21 cell isolation methods including complement-mediated lysis, flow cytometry,  
22 magnetic bead separation, panning, charge flow separation, laser  
23 microdissection and cell culture methods that promote selective propagation  
24 of cells to be enriched.

25 Each cell enrichment method may be performed alone or in  
26 combination with one or more other methods to thereby achieve a desired  
27 level of cell enrichment or purity.

1 Additional treatments may be utilized that facilitate cell isolation and  
2 enrichment, for example in one embodiment protease treatment (e.g.  
3 trypsin digestion) of cervical samples may be performed prior to density  
4 gradient enrichment.  
5

### 6 **5.1 Cell enrichment/isolation**

7 It will be appreciated that fetal cell enrichment may be achieved  
8 using physical characteristics such as size, granularity and/or using  
9 antibodies directed to fetal antigens not expressed, or expressed at low  
10 levels, by maternal cells.

11 Alternatively, fetal cells may be enriched by virtue of their non-  
12 expression of maternal or non-fetal antigens.

13 Accordingly, fetal cell enrichment may be performed by negative  
14 depletion of maternal cells and/or positive selection of fetal cells according  
15 to antigen expression.

16 Antigens that may be applicable to antibody-based enrichment  
17 include, but are not limited to, CD71,  $\gamma$  globin (fetal) and  $\zeta$  globin  
18 (embryonic), glycophorin A, CD36, Fki-1, EPO-R, CDw50, CD45, human  
19 chorionic gonadotrophin (HCG), placental alkaline phosphatase, human  
20 placental lactogen (FD0202N), folate binding protein (LK26) and HLA  
21 antigens such as HLA-Class II, for each of which specific antibodies are  
22 readily available.

23 Preferred antigens are human placental lactogen (FD0202N) and  
24 folate binding protein (LK26).

25 In the broadest sense, antibody-based enrichment may utilize any  
26 technique that selects cells (*i.e* positive selection) or depletes cells (*i.e*  
27 negative selection) according to antigen expression or non-expression, as



1 the case may be. A non-exhaustive list includes panning, complement-  
2 mediated lysis, fluorescence-activated cell sorting (FACS) and magnetic  
3 activated cell sorting (MACS).

4 It will also be appreciated that the aforementioned techniques may  
5 be used alone or in sequential combination to enrich fetal cells.

6 Preferred methods utilize FACS. FACS can enrich samples by using  
7 physical cellular characteristics including but not limited to size, shape,  
8 granularity and the like and/or fluorescently labelled antibodies.

9 For FACS enrichment, fluorescently-labeled antibodies are bound to  
10 the cells of interest. These cells are then passed through the excitation laser  
11 in a single cell stream and measured for size, granularity and fluorescent  
12 activity. Specific parameters are set and cells that fall within those  
13 parameters (e.g. fluorescence, forward light scatter, side scatter) are  
14 collected by a cell sorter into receptacles such as 96 or 384 well plates to  
15 facilitate high throughput.

16 In a preferred embodiment, fetal cells are enriched by FACS using  
17 antibody to placental lactogen, trypsin release of bound beads followed by  
18 FACS enrichment using antibody to folate binding protein (LK26).

#### 19 20 Charge Flow Separation

21 Charge flow separation uses dielectrophoretic forces which occur on  
22 cells when a non-uniform electrical field interacts with field-induced  
23 electrical polarization. Depending on the dielectric properties of the cells  
24 relative to their suspending medium, these forces can be positive or  
25 negative, directing the cells toward strong or weak electrical field regions.  
26 Because cells of different types or in distinct biological states have different  
27 dielectric properties, differential dielectrophoretic forces can be applied to

1 drive their separation into purified cell populations (Wang *et al.*, 2000.  
2 Analytical Chemistry **72** 832-839).

3  
4 Fetal cells may be enriched by selective growth in the presence of  
5 appropriate cytokines and culture conditions that favor the selective  
6 proliferation of fetal progenitor cells over maternal cells. Selective growth  
7 may be performed after initial isolation or enrichment by one or more other  
8 enrichment methods.

9 For example, fetal nRBC's (nucleated red blood cells) may be cultured  
10 after gradient enrichment and/or MACS enrichment in culture media  
11 containing many fetal NRBC growth factors (Bohmer *et al.*, 1998, Br J  
12 Haematol **103** 351-360). It is also contemplated that culture with fetal  
13 NRBC growth factors may stimulate a much higher basal proliferative  
14 capacity than mature progenitor cells and that this can be enhanced by  
15 addition of cytokine cocktails such as flt-3 ligand and thrombopoetin  
16 (Holzgreve *et al.*, 2000, Baillieres Best Pract Res Clin Obstet Gynaecol **14**  
17 709-722).

18 In light of the foregoing, a preferred embodiment of the invention  
19 provides a method of fetal cell isolation and analysis including the steps  
20 of:

21 (i) improved high throughput enriching of fetal cells from a Pap  
22 smear sample according to physical and/or fluorescent characteristics where  
23 at least one antibody binds to a fetal cell antigen.

24 Preferably, step (i) includes the sequential steps of:

25 (a) protein digest to release cellular mixture into discrete cells  
26

(b) using FACS to determine and separate fetal cells by physical characteristics

(c) using FACS to determine and separate fetal cells based on fluorescent characteristics using antibodies such as placental lactogen;

(ii) Improved high throughput amplification of nucleic acid product from pooled or single cells using a generic kit such as Genomiphi.

(iii) Genetic identification of sample using DNA fingerprinting. Genetic identification can be undertaken using STR profiling as previously published (Findlay *et al.*, 1997, Nature **389** 355-356)

(iv) Genetic analysis using a variety of non-limiting techniques such as RT-PCR, CGH, FISH, multiplex PCR, SNP analysis, and/or simultaneous analysis of any combination of above.

Preferably, step (iv) includes the sequential steps of:

(a) High throughput genetic analysis

(b) Detection of genetic product

Improved high throughput automated data processing to create analysis report. Analysis reports can include indicators of diagnosis/screening markers disease status as well as factors such as cell origin. Automated analysis provides the capacity to analyse many millions of analyses parameters extremely quickly and thus provide high throughput analysis.

The combination of each of the incremental improvements in the above steps allow high throughput processing and analysis of fetal samples

1 Other uses of enriched cells is for subsequent genetic analysis,  
2 biochemical analysis, morphological analysis, histology, cytology, cell  
3 culture and the like.

## 4 **5.2 Genetic analysis**

5 A more preferred use is for genetic analysis.

6 As used herein, "*genetic analysis*" and "*genetic diagnosis*" are used  
7 interchangeably and broadly cover detection, analysis, identification and/or  
8 characterization of isolated genetic material and includes and encompasses  
9 terms such as, but not limited to, genetic identification, genetic diagnosis,  
10 genetic screening, genotyping and DNA fingerprinting (also commonly  
11 known as STR profiling) which are variously used throughout this  
12 specification.

13 The term "*nucleic acid*" as used herein designates single-or double-  
14 stranded mRNA, RNA, cRNA, RNAI and DNA inclusive of cDNA, genomic DNA  
15 and DNA-RNA hybrids.

16 A "*polynucleotide*" is a nucleic acid having eighty (80) or more  
17 contiguous nucleotides, while an "*oligonucleotide*" has less than eighty (80)  
18 contiguous nucleotides.

19 A "SNP" is a single nucleotide polymorphism.

20 A "*primer*" is usually a single-stranded oligonucleotide, preferably  
21 having 12-50 contiguous nucleotides which, for example, is capable of  
22 annealing to a complementary nucleic acid "template" and being extended  
23 in a template-dependent fashion by the action of a DNA polymerase such as  
24 *Taq* polymerase, RNA-dependent DNA polymerase or Sequenase™.

25 By "*genetic marker*" or "*marker*" is meant any locus or region of a  
26 genome. The genetic marker may be a coding or non-coding region of a  
27 genome. For example, genetic markers may be coding regions of genes,

1 non-coding regions of genes such as introns or promoters, or intervening  
2 sequences between genes such as those that include polymorphisms (such  
3 as single nucleotide polymorphisms), tandem repeat sequences, for  
4 example satellites, microsatellites, short tandem repeats (STRs) and  
5 minisatellites, although without limitation thereto.

6 A "probe" may be a single or double-stranded oligonucleotide or  
7 polynucleotide, suitably labeled for the purpose of detecting complementary  
8 sequences in Northern or Southern blotting, for example.

9 Genetic analysis may be performed by any method including, but not  
10 limited to, fluorescence *in situ* hybridization (FISH), primed *in situ* synthesis  
11 (PRINS) and nucleic acid sequence amplification, preferably in the form of  
12 multiplex fluorescent PCR amplification (MFPCR).

13 Examples of fluorescent *in situ* hybridization (FISH) and Primed In  
14 Situ Synthesis (PRINS) may be found in Findlay *et al.*, 1998, J. Assisted  
15 Reproduction & Genetics **15** 257.

#### 16 **5.2.1 Multiplex fluorescent PCR**

17 As used herein, "multiplex amplification" or "multiplex PCR" refers to  
18 amplification of a plurality of genetic markers in a single amplification  
19 reaction.

1 MFPCR has been shown to be a reliable and accurate method for  
2 determining sex (Salido *et al.*, 1992, *Am. J Human genetics* **50** 303; Findlay  
3 *et al.*, 1994a, *Human Reproduction*, **9** 23; Findlay *et al.*, 1994b, *Advances in*  
4 *Gene Technology: Molecular Biology and Human Genetic Disease*. Vol 5,  
5 page 62. Findlay *et al.*, 1995, *Human Reproduction* **10** 1005-1013; Findlay  
6 *et al.*, 1998c, *supra*) diagnosing genetic diseases such as cystic fibrosis  
7 (Findlay *et al.*, 1995, *supra*), detecting chromosomal aneuploidies and in  
8 genetic analyses for genetic identification, such as typically referred to as  
9 DNA fingerprinting (Findlay *et al.*, 1997, *Nature* **389** 355-356).

10 With regard to genetic markers for genetic analysis, preferred genetic  
11 markers are STR and/or SNP markers. International Application  
12 PCT/AU02/01388 provides an extensive array of STR markers and primers  
13 together with MFPCR methodology to successfully amplify multiple STR  
14 markers from limiting amounts of nucleic acid template.

15 Although from the foregoing a preferred method of genetic analysis is  
16 PCR, nucleic acid sequence amplification is not limited to PCR.

17 Nucleic acid amplification techniques are well known to the skilled  
18 addressee, and also include ligase chain reaction (LCR) as for example  
19 described in Chapter 15 of Ausubel *et al.* *CURRENT PROTOCOLS IN*  
20 *MOLECULAR BIOLOGY* (John Wiley & Sons NY, 1995-1999); strand  
21 displacement amplification (SDA) as for example described in U.S. Patent  
22 No 5,422,252; rolling circle replication (RCR) as for example described in  
23 Liu *et al.*, 1996, *J. Am. Chem. Soc.* **118** 1587 and International application  
24 WO 92/01813 and by Lizardi *et al.*, in International Application WO  
25 97/19193; nucleic acid sequence-based amplification (NASBA) as for  
26 example described by Sooknanan *et al.*, 1994, *Biotechniques* **17** 1077; and

1 Q- $\beta$  replicase amplification as for example described by Tyagi *et al.*, 1996,  
2 Proc. Natl. Acad. Sci. USA **93** 5395.

3 The abovementioned are examples of nucleic acid sequence  
4 amplification techniques but are not presented as an exhaustive list of  
5 techniques. Persons skilled in the art will be well aware of a variety of other  
6 applicable techniques as well as variations and modifications to the  
7 techniques described herein.

8 As used herein, an "*amplification product*" refers to a nucleic acid  
9 product generated by a nucleic acid amplification technique.

10 Although the invention also contemplates use of nucleic acid other  
11 than DNA, preferably the nucleic acid is DNA.

12 More preferably, the nucleic acid is genomic DNA.

13 Isolation of cellular nucleic acids is well known in the art, although  
14 the skilled person is referred to Chapters 2, 3 and 4 of Ausubel *et al.*  
15 CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley & Sons NY,  
16 1995-1999), for examples of nucleic acid isolation.

### 17 **5.2.2 SNP analysis**

18 Single Nucleotide Polymorphisms (SNP) are the most frequent form of  
19 variation found in the genome, estimated to occur every 1000 bases. SNP  
20 genotyping has multiple applications such as predictive medicine, personal  
21 medicine, forensic identification and pharmacogenomics. SNP genotyping  
22 has already been used to investigate a number of disorders such as cystic  
23 fibrosis, Factor V Leiden mutation, and factors such as A, B, O and Rh blood  
24 grouping. However conventional SNP analysis is limited by the relatively  
25 high amount of extracted DNA usually required (up to 100ng) for analysis.  
26 However in genomic analysis, there is increasing demand to both maximize  
27 data by performing multiple analyses and secondly to analyze minimum

1 amounts of sample, even to the single cell level. Although multiple SNP  
2 analyses can be performed routinely, the degree of sensitivity is still far from  
3 single cell level analysis. Multiplex single cell SNP analysis has been  
4 problematic and again is not amenable to the high throughput processing  
5 required of clinical application.

6 Preferred sources of nucleic acids are mammals, preferably humans.

7 The invention also contemplates genetic analysis of non-human  
8 samples such as from cows, sheep, horses, pigs and any other mammal  
9 including companion animals, sporting animals and livestock, although  
10 without limitation thereto.

11 So that the invention may be readily understood and put into  
12 practical effect, reference is made to the following non-limiting examples.  
13

## 14 **6 MATERIALS AND METHODS**

15

### 16 **6.1 Fetal cell Isolation**

17 Informed consent was obtained from pregnant women between 7 and 31  
18 weeks gestation. A pap smear cervix brush (Rovers Medical Devices,  
19 Lekstraat, The Netherlands) was inserted through the external os to a  
20 maximum depth of two centimeters. The brush was then removed whilst  
21 rotating a full turn. The material that was caught on the brush was smeared  
22 on a slide which was used for routine cervical cancer screening. The  
23 remaining material on the brush was included in the study. Some pregnant  
24 women were undergoing pregnancy termination immediately after the pap  
25 smear sample was taken, and in these cases the pap smear sample was not  
26 used for routine cervical screening and the entire sample was available for  
27 analysis.



1 Cells were washed off the cervix brush into Dulbeccos PBS  
2 (Invitrogen, Melbourne Australia). The cells were then spun at 402g in a  
3 Sigma 4K15 centrifuge (Sigma, St Louis, USA), the supernatant was poured  
4 off and the remaining material transferred to a 1.5mL centrifuge tube. The  
5 cells were then spun at 3000rpm in a biofuge pico (Kendro, Ashville, North  
6 Carolina), the supernatant was then poured off and the cells were  
7 resuspended in 800uL PBS. A buccal swab was also taken from the mother  
8 to provide an uncontaminated source of maternal cells.

## 9 **6.2 Trypsin Digestion**

- 10 - 3 X 200uL + 1 X 50uL cell suspension from each sample
- 11 - 200uL (or 50uL) 2.5% Gibco Trypsin/EDTA in PBS was added
- 12 - Incubated 37 degrees for 2 hours
- 13 - 1mL PBS was added and then centrifuged 3000rpm 5 minutes
- 14 (Biofuge pico)
- 15 - Supernatant was removed
- 16 50uL Initial material sample was placed in -20°C freezer for later analysis

## 18 **6.3 Isolation of fetal cells by physical characteristics using** 19 **FACS**

- 20 1. Cells should be washed 2-3x with FACS buffer (PBS  
21 supplemented with either 1% BSA or 5% FBS and  
22 containing 0.05% NaN<sub>3</sub>).
- 23 2. Suspend the cell pellet from the final wash in 50 microliters  
24 FACS buffer (or more if more than one analysis is to be  
25 done on a single sample).
- 26 3. Incubate for 30 minutes on ice.

1                   4. Wash cells 2-3x with FACS buffer and suspend in 200-300  
2                   microliters FACS buffer for analysis.

3                   Fetal cells may be isolated by any of the aforementioned cell isolation  
4                   methods.

5                   In all cases samples from non-pregnant women are run as control  
6                   cases to determine the base-line level of non-specificity.

7                   Preferably, said one or more fetal cells are isolated by FACS sorting.

8                   Said one or more fetal cells may be isolated from any pregnant  
9                   mammal.

10                  Preferably, said one or more fetal cells are isolated from a pregnant  
11                  human.

12                  When a fetus is at increased risk for genetic defects such as  
13                  chromosomal anomalies, prior art prenatal diagnosis is by invasive  
14                  procedures such as either chorionic villus sampling (CVS) in the late 1<sup>st</sup>  
15                  trimester or amniocentesis in the 2<sup>nd</sup> trimester of pregnancy. By the third  
16                  trimester, a combination of CVS and amniocentesis, or even fetal blood  
17                  sampling, may be necessary.

18                  A rapid, less-invasive and low cost method of prenatal diagnosis  
19                  involves genetic diagnosis from fetal cells shed into the cervical sump at 6-  
20                  20 weeks of gestation. These samples are obtained from the cervix by  
21                  cytobrush in a manner identical to a PAP smear, which is similar to but  
22                  significantly less invasive than invasive transcervical sampling.

23

1           Although promising, previous work has identified several major  
2 difficulties. Firstly the need to obtain the large numbers of fetal cells  
3 required for genetic diagnosis. Secondly the isolation of fetal cells from the  
4 cervical sample is extremely difficult as recent results suggest that fetal  
5 cells could be isolated and diagnosed in only ~22% of cases due to the  
6 presence of "contaminating" maternal cells. Previous approaches have  
7 generally concentrated on isolating fetal cells by morphology or cell sorting.  
8 Unfortunately, morphology grading is extremely time-consuming, expensive  
9 and generally unreliable and inaccurate. Alternative cell sorting techniques  
10 involves antibody-labelled slides to capture fetal cells, which is generally  
11 unspecific resulting in major maternal contamination and misdiagnosis or  
12 insufficient fetal cells. Thirdly the difficulty in positively identifying the  
13 isolated cell as being fetal rather than maternal; previous approaches have  
14 determined male fetal cells which identifies the fetus as the mother is  
15 female but female signals could either indicate female cells or maternal  
16 contamination and thus misdiagnosis.

17           Fourthly the difficulty of obtaining genetic diagnosis from small cell  
18 numbers. Although fetal cells have been identified in cervical samples  
19 (mainly by identifying male cells within the sample) aneuploidy screening  
20 (the primary reason for prenatal diagnosis) cannot usually be performed nor  
21 diagnosis made if the fetus is female due to the risk of contamination  
22 causing misdiagnosis.

23           Finally, although PAP sampling collection is theoretically much safer  
24 than CVS and amniocentesis as PAP smears have been taken during  
25 pregnancy for many years, relative safety remains to be fully evaluated.

1           According to the present invention, it is preferred that said fetal cells  
2 are present in a maternal uterine cavity or endocervical canal sample,  
3 particularly a transcervical sample. Methods of isolating fetal cells include  
4 cervical cotton swab, cytobrush, aspiration of cervical mucus, lavage of the  
5 endocervical canal and uterine lavage. Samples can be obtained from  
6 transcervical aspiration of mucus from just above the internal os or the  
7 lower uterine cavity. Lavage is generally conducted with a saline wash, but  
8 other isotonic solutions are suitable. Typically, endocervical lavage with 5-  
9 10ml or intrauterine lavage with 10-20ml saline provides sufficient fetal  
10 cells upon separation from maternal cells. The sample may be collected  
11 using a combination of methods.

12           Preferably, cell samples are isolated from a female human in the first  
13 trimester of pregnancy or when the fetus is between 6 to 17 weeks  
14 gestation. The sample can be in any solution which maintains cell integrity  
15 and minimizes cell lysis or damage, preferably a physiological solution, or  
16 more preferably, a saline solution or tissue culture medium with or without  
17 the addition of sera.. The sample is preferably stored at 0°C to 4°C until use  
18 to minimize the number of dead cells, cell debris and cell clumps.

19           Preferably, to aid fetal cell separation, clumps of cells are preferably  
20 treated to obtain a suspension of single cells. The clumps may be separated  
21 by techniques known to a skilled person, such as enzymatic, chemical or  
22 mechanical separation. For example, enzymatic separation may utilise  
23 protease or trypsin. Chemical separation may utilise acetyl cysteine and  
24 mechanical separation may involve gentle teasing, aspiration or  
25 micromanipulation.

26           The number of fetal cells in the sample varies depending on factors  
27 including the age of the fetus, method of sampling, number and frequency

1 of samplings, the vigour of sampling and the volume aspirated.

2 Maternal uterine cavity or endocervical canal samples typically  
3 contain at least two main types of nucleated fetal cells: cytotrophoblasts  
4 and syncytiotrophoblasts cells.

5 Fetal cells can be isolated either by selecting fetal cells from maternal  
6 cells (positive selection) or isolating the maternal cells from the fetal cells  
7 (negative selection) or most preferably a combination of both. Preferably,  
8 the nucleated fetal cells are retained in the purified sample.

9 Preferably, the maternal cells are labelled with an antibody for a  
10 selected maternal antigen. In that case, fifty percent of the time, the  
11 sample will contain unlabelled fetal cells. Preferably, the maternal cells are  
12 double-labelled. When the selected maternal antigens are encoded by  
13 alleles of different genetic loci, three out of four times, fetal cells are  
14 unlabelled or single-labelled depending on whether the fetus inherits one or  
15 neither of the maternal alleles. When the selected maternal antigens are  
16 encoded by alleles of the same genetic locus, fetal cells are single-labelled.  
17 The separation procedure is described below using double-labelled maternal  
18 cells.

19 Suspension media, use of protein supplements such as 5-10% BSA or  
20 HSA and appropriate cell concentrations for FACS-based separation are well  
21 known in the art and described in references such as Practical Flow  
22 Cytometry *supra* and Current Protocols in Immunology Eds Coligan *et al.*,  
23 *supra*.

24 More preferred as a protein supplement is about 5% autologous  
25 plasma, which can be harvested from a purified blood sample and is non-  
26 immunogenic.

1           The cells of the blood sample, preferably purified cells, are labelled  
2 with fluorescent antibodies specific for the antigens encoded by at least one  
3 maternal polymorphic locus, selected as described previously. The  
4 antibodies can be polyclonal or monoclonal, preferably monoclonal.  
5 Preparation of polyclonal and monoclonal antibodies for an antigen of  
6 interest is well known. Furthermore, there is a vast supply of potentially  
7 useful antibodies, such as to human HLA antigens, that are commercially  
8 available or available from hybridoma depositories such as the ATCC.

9           For example, in the case of separation using HLA antigens, HLA  
10 antigen-specific antibodies are commercially available. Typically the HLA  
11 Class 1 loci (A, B and C) and the Class 11 DR and DQ loci are determined by  
12 serological methods. Therefore, antibodies specific for those antigens are  
13 readily available. Sources of HLA antigen-specific antibodies include Genetic  
14 Systems (Seattle, Wash.) and C6 Diagnostics (Mequon, Wis.). Blood group  
15 antigens are also determined serologically and the antibodies are  
16 commercially available.

17           The antibody is labelled with a dye that facilitates, cell sorting,  
18 particularly a fluorochrome, Suitable dyes for FACS analysis and/or  
19 separation are well known in the art. Examples of dyes are described in  
20 Practical Flow Cytometry (Second Edition), *supra*, at pages 115-198 and in  
21 Chapter 5 of Current Protocols in Immunology, *supra*. Preferred dyes are  
22 fluorochromes including fluorescein (e.g., fluorescein isothiocyanate--FITC),  
23 rhodamine (e.g., tetramethylrhodamine isothiocyanate--TRITC),  
24 phycoerythrin (PE), allophycocyanin (APC) and Texas Red (Molecular  
25 Probes, Eugene, Oreg.).

26           For four-color flow cytometric sorting, cells can be labelled with  
27 antibodies for antigens expressed by four alleles. In that case, preferably,

1 the antibodies are specific for both antigens expressed by the alleles of two  
2 maternal HLA loci. Maternal cells are labelled with all four fluorochromes.  
3 Fetal cells are labelled with two of the four fluorochromes when none of the  
4 nontransmitted maternal alleles is inherited from the father. By using four  
5 fluorochromes from two loci, the fetal cells remain distinguishable from the  
6 maternal cells even when the fetus inherits one of the nontransmitted  
7 maternal alleles from the father. A second staining is only necessary when  
8 the fetus inherits both nontransmitted maternal alleles from the father.  
9 When the antibodies are for antigens expressed by three or four maternal  
10 loci, using the additional dyes increases the likelihood that the fetus did not  
11 inherit each of the maternal alleles.

12 Fetal cells are only indistinguishable from maternal cells by the  
13 method of the present invention in the case where the fetus inherits all six  
14 non-transmitted maternal alleles from the father.

15 For antibody labeling, cells are preferably incubated at about 4°C to  
16 maintain cell integrity. Incubation for about 30 minutes at 4°C is usually  
17 sufficient for substantially complete antibody binding. The sample is  
18 preferably mixed, as by using a hematology blood rocking device, during  
19 the incubation to ensure contact of the antibodies with the cells. Preferably,  
20 the incubation is performed in the dark when using a fluorochrome label.  
21 Secondary reactions (e.g. incubation of fluorochrome-labelled avidin with  
22 biotin labelled cells) are performed in the same manner.

23 In a preferred embodiment, an additional selection criterion is DNA  
24 content. Fetal cells having greater than 2C DNA content can be determined  
25 using a number of vital-staining fluorochromes such as the Hoechst dyes,  
26 DAPI (4-6-diamidino-2-phenylindole), hydroethidine and 7-  
27 aminoactinomycin D (7AMD). The fluorochrome used depends on the labels

1 used to select the fetal cells. A second laser capable of emitting UV light is  
2 required to excite Hoechst and DAPI dyes. Each of the above-described  
3 dyes can be used with FITC and PE.

4 The ability of the cell sorter to separate maternal and fetal cells  
5 ultimately depends on the percentage of fetal cells in the sample. To obtain  
6 a fetal cell sample that is at least about 60% pure (60% of the sorted cells  
7 are fetal cells), the fetal cells should constitute about 0.001% of the  
8 maternal cells or greater. Preferably, the sample contains 80%, more  
9 preferably 90% fetal cells post-sorting.

10 When 100% purity is desired, the sorted cells can be plated for  
11 subsequent analysis. For example, cell suspensions containing an individual  
12 cell can be isolated within a preselected volume of suspension medium by  
13 limiting dilution. Drops containing individual cells can then be placed in  
14 suitable pre-made containers (e.g. 96 well plates) for subsequent nucleic  
15 acid amplification and/or analysis.

16 For PCR analysis, analysis can be performed using a single,  
17 unambiguously identified fetal cell.

18 Alternatively, ways can be envisaged of identifying monozygosity  
19 (indicative of the presence of a monogenic disease) in a mixed cell  
20 population containing minimal fetal material including as few as one fetal  
21 cell in ten cells. Following sorting, the separated cells can be washed twice  
22 in a physiologic buffer and resuspended in an appropriate medium for any  
23 subsequent analysis to be performed on the cells.

24 Following the present recovery method, whether based on solid phase  
25 (eg. magnetic beads or panning) or FACS separation, the fetal cells can be  
26 used in the same manner as fetal cells obtained by other methods such as  
27 amniocentesis and chorionic villus biopsy. The cells can be used as a source



1 of DNA for analysis of the fetal alleles, as by polymerase chain amplification.  
2 PCR analysis methods may be used to detect, for example, fetal sex, beta -  
3 thalassemia, phenylketonuria (PKU), and Duchennes muscular dystrophy.

4 Alternatively, the cells can be cultured in the same manner as biopsy  
5 materials for karyotyping analyses. However, the incubation period may be  
6 significantly shortened if a DNA content of greater than or equal to 2C is  
7 used as a selection criterion.

#### 8 9 **6.4 Isolation of antibody labelled fetal cells by FACS**

10 Samples were placed through the following protocol:  
11

- 12 1. 10 minutes in 10% Donkey serum (Sigma-Aldrich, St.  
13 Louis, USA) diluted in PBS
- 14 2. Donkey serum was removed
- 15 3. 100uL of each of the following Primary Antibodies, 1/100  
16 dilution in 10% donkey serum (*i.e.* final dilution 1/200) was  
17 then added.
- 18 4. ab7816 Rabbit anti-human chorionic gonadotrophin  
19 antibody (Abcam, Cambridge, UK) and NCL-PLAP Mouse  
20 anti- placental alkaline phosphatase antibody (Novocastra  
21 Laboratories, Newcastle, UK).
- 22 5. Samples were then incubate 90 minutes at room  
23 temperature in humidified chamber
- 24 6. Samples were then washed 3 X 5 minutes in PBS
- 25 7. 100uL of each following Secondary antibody 1/200 dilution  
26 in PBS (*ie* final dilution 1/400) was then added.

8. Donkey FITC polyclonal to rabbit IgG (Abcam, Cambridge, UK) and Chicken Rhodamine polyclonal to mouse IgG (Abcam, Cambridge, UK).

9. Samples were then incubated 45 minutes at room temperature in humidified chamber

10. Samples were then washed 2 X 5 minutes PBS

In all cases samples from non-pregnant women are run as control cases to determine the base-line level of non-specificity.

To improve the accuracy, reliability and cost effectiveness of non-invasive prenatal genetic diagnosis from pap smears, it is necessary to develop enrichment strategies that both reduce the concentration of contaminating cells and secondly recover as many fetal cells as possible. The use of digesting enzymes such as trypsin or collagenase increase the number of fetal cells retrieved.

In one embodiment, genetic analysis of fetal cells isolated from pap smears preferably requires a number of serial enrichment strategies in order to provide a reliable source of relatively uncontaminated fetal cells. Initial FACS enrichment strategies usually identify cells using physical characteristics such as density, charge or size. Although single cycles are not highly specific they do reduce target cell loss and are relatively low in cost, therefore multiple cycles, either on physical or fluorescent characteristics, are utilised to maximise specificity whilst maintaining cellular yield. Secondary enrichment strategies such as antibody staining will often identify cells using specific cellular traits. Primary and secondary enrichment strategies must work in unison to provide a reliable source of uncontaminated fetal cells yet achieve maximum yield. Performing multiple

cycles to improve purity and/or yield are not significant time or sample limiting steps.

### **6.5 Cell processing**

Cells were isolated by the FACS machine into 96 well plates containing 1uL lysis buffer (200mM potassium hydroxide/50mM Dithiothretol), and incubated at 65°C for 10 minutes. 1uL neutralising buffer (300mM KCl/900mM Tris-HCl pH8.3/200mM HCl) [Cui, 1989] was then added. Cells were stored at -80°C until MFPCR.

### **6.6 Genetic identification using DNA fingerprinting**

Multiplex fluorescent PCR of Amelogenin and STRs listed in Table 1 or more preferably listed in Table 3, D3S1358, D5S818, D7S820 and CSF1PO THO, D21S11, D18S51, VWA, FGA, D3S1358, D5S818, D7S820, CSF, TPOX was performed on isolated cells. Each reaction contained forward and reverse primers, 1 X PCR buffer (Applied Biosystems, USA), 1.5mM MgCl<sub>2</sub> (Applied Biosystems, USA), 1.25mM each dNTP (Gibco, Life Technologies, Melbourne, Australia) and 1 unit HotStart Taq (Qiagen, Australia). PCR conditions were 94°C for 2 minute denaturation followed by 45 cycles of 94°C/10 second denaturation, 57°C/1 minute annealing and 68°C/30 second extension.

PCR product was processed using Ammonium acetate/Ethanol Clean-up. Post clean-up processing involved adding 2uL of cleaned-up product to 3uL loading buffer (Amersham Biosciences, Piscataway, New Jersey). Samples were then heated to 90 degrees for 60 seconds and placed immediately on ice. Analysis was completed using the Megabace 1000 capillary electrophoresis system with Genetic Profiler Version 1.5 software (Amersham Biosciences, Piscataway, New Jersey). Injection parameters

1 were -3kV for 45 seconds and run parameters were -10kV for 75 minutes  
2 at 44°C.

3 The procedure to identify a fetal signal within that produced by  
4 MFPCR of the isolated cells was that outlined in the paper 'Analysis and  
5 interpretation of mixed forensic stains using DNA STR profiling' (Clayton *et*  
6 *al.*, 1998, Forensic Science International **91** 55-70). That is the STR is an  
7 additional band to that found in the maternal fingerprint i.e. consistent with  
8 maternal signal. It is not consistent with a stutter band or artefact peak and  
9 that it is the same base pair size as bands identified as fetal for the same  
10 locus within other isolations from the same patient.

11 Protocols for enrichment and diagnosis of fetal cells from the cervix must  
12 be consistently successful, robust and inexpensive if the techniques are to  
13 become an alternative to invasive procedures such as amniocentesis or  
14 chorionic villus sampling. Previous inventions and work has been  
15 significantly limited by a variety of factors including: obtaining sufficient  
16 cells; isolation of fetal cells from the sample; genetic identification of cells  
17 to determine fetal source; genetic diagnosis from small cell numbers and  
18 sample collection.

19 Where previous work has failed to detect and analyse fetal cells at a  
20 consistent and reliable enough level to be considered as a promising tool  
21 towards minimally invasive prenatal diagnosis, this invention provides  
22 incremental improvements to multiple steps and combines them into a high  
23 throughput method allowing widespread application for the first time.

24 However alternatively it should also be appreciated that this invention  
25 may also be considered as a complementary technique to other non-  
26 invasive or minimally invasive tests such as biochemical screening and

1 ultrasound screening offered to pregnant women during the first trimester  
2 of pregnancy (Daryani *et al.*, 2000, J. Obstet. Gynecol. **183** 752).

3 Our results indicate that cells reacting against multiple antibody sets  
4 are present in all patients. The percentage of fluorescent cells vary, with no  
5 apparent correlation to gestation. The overall number of fluorescent cells in  
6 the sample also varies with no correlation to gestation. This may indicate  
7 that variation in the number of fetal cells in the sample is specific to the  
8 patient or perhaps more likely due to variations in the technique used by  
9 the operator performing the retrieval.

10 DNA fingerprinting using MFPCR was used to confirm cell origin of the  
11 fluorescent cells from each antibody set and patient. This MFPCR technique  
12 has the advantage of being highly discriminating for cell origin even when  
13 applied to very close relatives such as mother and baby.

14 Combining the antibody and MFPCR data from all patients, it is  
15 possible to determine a minimum specificity for each antibody set towards  
16 fetal cells although this may be due to non-specific binding to non-cellular  
17 particles, binding to non-intact cells or strong binding to a maternal cell  
18 lineage.

### 19 **6.7 STR Genetic analysis**

20 Previous work using genetic diagnosis of limited numbers of fetal cells  
21 obtained from the uterine cervix using techniques such as FISH and PCR is  
22 very limited (methods are compared in Table 4). FISH analysis can only  
23 identify fetal cells if they are aneuploid or originate from a male fetus  
24 (Fejgin *et al.*, 2001, *supra*) - this is an important and considerable  
25 limitation to the use of such techniques for prenatal diagnosis. Other studies  
26 use PCR analysis to detect disorders however in most cases this is limited to  
27 the gene analysed and quantitative variations in the maternal and fetal

1 alleles, for example RH(D) analysis (Tutschek *et al.*, 1995, Prenatal  
2 Diagnosis **15** 951). Again this is an important and considerable limitation to  
3 the use of such techniques for prenatal diagnosis.

4 However MFPCR has the advantages of overcoming these limitations,  
5 as it is not limited by sex or individual gene alleles. MFPCR has an  
6 extremely high level of discrimination between closely related individuals,  
7 can be performed on single cells and provides multiple diagnoses within a  
8 single reaction.

9 In this embodiment, MFPCR was used to accurately determine the  
10 presence of fetal cells in a mixed fetal/maternal sample. For these reasons  
11 we suggest that MFPCR be considered the preferred method of choice when  
12 performing prenatal genetic diagnosis from pap smear samples.

13 Multiplex fluorescent PCR of Amelogenin and STRs D3S1358,  
14 D5S818, D7S820, CSF1P0, TH0, FGA, D21S11, and D18S51 or any markers  
15 listed in Table 1, or more preferably Table 2, was performed on isolated  
16 cells using previously described protocols (Findlay *et al.*, 2001, *supra*;  
17 International Application PCT/AU02/01388). Each reaction contained  
18 forward and reverse primers, 1 X PCR buffer (Applied Biosystems, USA),  
19 1.25mM each dNTP (Gibco, Life Technologies, Melbourne, Australia) and 1  
20 unit Qiagen HotStarTaq (Qiagen Melbourne, Australia). PCR conditions were  
21 94°C/2 minute denaturation followed by 45 cycles of 94°C/10 second  
22 denaturation, 57°C/1 minute annealing and 68°C/30 second extension. The  
23 PCR uses no oil overlay, as the heated lid of the PCR is sufficient. The PCR is  
24 taken off the block and stored at 4°C until required for electrophoresis.

25 PCR product was processed using Ammonium acetate/Ethanol Clean-  
26 up. Post clean-up processing involved adding 2uL of cleaned-up product to  
27 3uL loading buffer (Amersham Biosciences, Piscataway, New Jersey).

1 Samples were then heated to 90 degrees for 60 seconds and placed  
2 immediately on ice. Analysis was completed using the Megabace 1000  
3 capillary electrophoresis system with Genetic Profiler Version 1.5 software  
4 (Amersham Biosciences, Piscataway, New Jersey). Injection parameters  
5 were -3kV for 45 seconds and run parameters were -10kV for 75 minutes  
6 at 44°C.

7 The procedure to identify a fetal signal within that produced from  
8 MFPCR of the isolated cells was that outlined in Clayton *et al.*, 1998, *supra*.

9 This embodiment also indicates that cells of fetal origin are indeed  
10 present in the endocervical canal of the mother. Due to the relatively low  
11 number of fetal cells present serial enrichment strategies must be utilized to  
12 in unison to provide a reliable source of uncontaminated fetal cells yet still  
13 provide maximum yield. Once a reliable source of fetal cells is established,  
14 the diagnostic techniques such as MFPCR used to screen these cells needs  
15 to not only confirm fetal origin and but also test for genetic traits.

16 Again MFPCR has the advantage of being highly discriminating for cell  
17 origin even when applied to close relatives such as mother and baby.  
18 MFPCR can be performed on single cells and provides multiple diagnosis  
19 within a single reaction. In this embodiment MFPCR was used to accurately  
20 determine the presence of fetal cells isolated from a mixed fetal/maternal  
21 sample.

22 This embodiment demonstrates that samples highly enriched in fetal  
23 cells (>90%) can be produced even though an uncontaminated source of  
24 fetal cells from pap smears (i.e. isolation of 100% fetal cells) may not be  
25 possible. Single fetal cells can then be easily isolated and used to screen for  
26 genetic traits. For this reason, and the ability to test for multiple probes,

MFPCR may be considered the method of choice when performing prenatal genetic diagnosis from pap smear samples.

### **6.8 SNP genetic analysis**

Many common diseases in humans are not caused by variation within single genes but are instead influenced by complex interactions among multiple genes as well as a multitude of environmental and lifestyle factors. Genetic factors may also confer susceptibility or resistance to a disease as well as determine the severity or progression of the disease. As most of the factors involved in these intricate pathways are unknown, it has therefore been difficult to develop screening tests for many diseases and disorders. It is therefore vital to understanding the genetic basis of common human diseases and this depends on a detailed understanding of the variability observed in the human genome.

Single Nucleotide Polymorphisms (SNP) are the most frequent form of variation found in the genome, estimated to occur every 1000 bases. SNP genotyping has multiple applications such as predictive medicine, personal medicine, forensic identification and pharmacogenomics. However conventional SNP analysis is limited by the relatively high amount of extracted DNA usually required (up to 100ng) for analysis. However in genomic analysis, there is increasing demand to both maximize data by performing multiple analyses and secondly to analyze minimum amounts of sample, even to the single cell level. Although multiple SNP analyses can be performed routinely, the degree of sensitivity is still far from single cell level analysis. Multiplex single cell SNP analysis has been problematic and again



1 is not amenable to the high throughput processing required of clinical  
2 application.

3 SNP genotyping can be used to identify genetic regions associated with a  
4 disease phenotype, allowing researchers to target particular areas of  
5 interest and begin to reveal relevant genes associated with a disease. SNP  
6 patterns from a large group of affected individuals can be compared to  
7 those of unaffected individuals. These association studies can detect  
8 differences in the SNP patterns of the two groups, thereby indicating  
9 potentially important SNPs and thus genetic regions for further study.  
10 Eventually SNP profiles that are characteristic of a variety of diseases will  
11 become established. Defining and understanding the role of genetic factors  
12 in disease will also allow researchers to better evaluate the role that non-  
13 genetic factors - such as behaviour, diet, lifestyle, and physical activity -  
14 have on disease.

15 SNP genotyping has already been used to investigate a number of  
16 disorders such as cystic fibrosis, Factor V Leiden mutation, and factors such  
17 as A, B, O and Rh blood grouping.

18 SNP genotyping is undertaken in six main stages: PCR, Post-PCR  
19 cleanup, SNP primer extension reaction, final cleanup, SNP product sizing  
20 and analysis.

21 To provide an example of SNP genotyping we have utilised methods based  
22 around Amersham Megabace 1000 SNP manufacturers protocols.

23

### 6.8.1 PCR for SNPs

Isolated fetal cells were processed in a multiplex SNP reaction consisting of oligonucleotides for specific SNPs such as Kell, Rh etc. Each 25 $\mu$ l reaction contained 25pmol forward and reverse primers, 1 X PCR buffer, 5mM each dNTP (Gibco, Life Technologies, Melbourne, Australia) and 1 unit Qiagen HotStarTaq (Qiagen, Melbourne, Australia). PCR conditions were 95°C for 15 minute denaturation followed by 45 cycles of 20 secs at 94°C, 60°C then 72°C then followed by a two minute extension at 72°C.

### 6.8.2 Post PCR cleanup

Post PCR cleanup removes excess dNTPs and residual primers before primer extension and commonly uses SAP (shrimp alkaline phosphatase) and EXOI (exonuclease I) protocols.

Using a half-reaction protocol, 10 $\mu$ l of PCR product is added to 2.5 $\mu$ l EXO SAP (Amersham Biosciences) and incubated at 37°C for 15 minutes.

### 6.8.3 SNP primer extension reaction

Combine 1.0  $\mu$ l SNuPe premix and 1 $\mu$ l dilution buffer (Amersham Biosciences) with 2 pmol extension primer, 1-10 ng cleaned PCR template (~1  $\mu$ l) with distilled water to bring up to a final volume of 5 $\mu$ l. PCR conditions were 25 cycles of 96°C for 10 sec, 50° C for 5 sec then 60° C for 10 sec.

#### 6.8.4 Final cleanup

The purpose of a final clean-up step is to remove excess terminators and desalts the samples prior to electrokinetic injection. AutoSeq96 columns (Amersham Biosciences) are used as per following protocol.

Spin product at 910g for 5 minutes, add 100 $\mu$ l deionised water, repeat spin, add samples to spin columns and repeat spin.

It is recommended to have at least one additional water wash to obtain sufficient yield good signal intensities. Additional water washes will further increase the signal intensity.

#### 6.8.5 SNP product sizing

Add 2.5ul multiple injection marker (MIM, Amersham Biosciences) to 497.5ul loading solution then dispense 5 $\mu$ l into each well. Load LPA matrix (Amersham, Biosciences) and rerun as per manufacturers protocol. Perform cycles of sample injection then two-minute electrophoresis interval and repeat upto twelve times.

Enter sizing and SNP parameters into Snupe and Instrument Control Manager. Analysis is performed using SNP Profiler as per manufacturers protocols.

## 7 Overview

This specific example of the invention demonstrates that high throughput enrichment of fetal cells from pap smears can be performed for the first time using combination of improved methods including FACS, nucleic acid amplification, genetic analysis. The combinations of this technology with improved automated procedures for genetic identification

1 and analysis, have been applied to create a much improved method which  
2 allows automated high throughput system to maximize cost effectiveness  
3 and thus offer practical non-invasive prenatal analysis application for the  
4 first time.

5 This embodiment therefore represents a substantial advance  
6 compared to prior art and confirms that non-invasive prenatal diagnosis  
7 from pap smears can be automated to provide the high through capability  
8 required for clinical application.

9 Throughout this specification, the aim has been to describe the  
10 preferred embodiments of the invention without limiting the invention to  
11 any one embodiment or specific collection of features. Various changes and  
12 modifications may be made to the embodiments described and illustrated  
13 herein without departing from the broad spirit and scope of the invention.

14 All patent and scientific literature, computer programs and algorithms  
15 referred to in this specification are incorporated herein by reference in their  
16 entirety.

7.1.1 TABLE 1 – STR markers used for DNA fingerprinting and genetic analysis

MARKER	ALIAS	GENBANK NO.	POSITION	PRIMER SEQUENCE
D13S241	UT556	L17673	13pter	CCA GGC ACT TTG GGA GGC TG ACC CAC TGT ATC CTG GGC A
D13S242	UT557	L18329	13q21.2	ATT GCA CCC CAT CCT GGG TCC TTT TCC TAC CAT TTG CAT
D13S243	UT558	L18330	13cen-13q12.1	ACT GTA CTT CTG CCT GGG C TTT TGT AAT GCC TCA ACC ATG
D13S248	UT1213	L15541	13q32-13q34	ACT TAA ATG TCC ATC AAT AAA T TGA TTG GCT TTT TTT ACT TAC
D13S251	UT1329	L16338	13q31-13q32	CAC ATA GCT TAT TGT TGT TGC GTT ATC TGT GAG CAA ATA CAG
D13S253	UT1378	L16396	13q22-13q32	CTC AAG GGA TGT TAA CAC AC AGG AGG AAA AAG TGG AGA AG
D13S254	UT1585	L18690	13q31-13q32	TGA ACT CCG GCC TGG GTG A TTT TGG AGC TGG GGA TGT C
D13S256	UT2120	L17977	13q14.1-13q22	CCT GGG CAA CAA GAG CAA A AGC AGA GAG ACA TAA TTG TG
D13S257	UT2119	L18729	13q14.1-13q21.1	CAA CAA GAG CAA AAC TCC AT AAG CAC ATA AGT TGG TAT GAA
D13S258	UT2413	L18095	13q21.2-13q31	ACC TGC CAA ATT TTA CCA GG GAC AGA GAG AGG GAA TAA ACC
D13S303	UT936	L31309	13q22-13q31	ACA TCG CTC CTT ACC CCA TC TGT ACC CAT TAA CCA TCC CCA
D13S631	UT7403	L18392	13q31-13q32	GGC AAC AAG AGC AAA ACT CT TAG CCC TCA CCA TGA TTG G
D18S51	UT574	L18333	18q21.33- 18q21.33	GAG CCA TGT TCA TGC CAC TG CAA ACC CGA CTA CCA GCA AC

D18S378	UT485	L16262	18p11.22- 18p11.22	AGC CTG GGT GAC AGA GCA A ACA GGG AAA GCT GGG GGA T CAT CCA TCC ATC CTT CCA C TGT GCT GGT ATT ACA GGC G TCA GGA GAA TCA CTT GGA AC TCC ATG AAG TAG CTA AGC AG TAA CCA AAG CAA ATC CCT GG CAC TTA CAC TGT TAT CCT GG CTG GTT TTC GTC TTG AGA AG CAC TAT TCC CAT CTG AGT CA CTT CCC TGG GTA TCA AGA CT TCC CAC TAT ATG TAT GTT CAC C GGC TGA GAC AGG AGA ATC AC CTC ACC AGG ATT TCC TTG C ACC ACA GTT ACT AAG ATG TAA GCC TCC AGA AAA AAT TTC CA CTG TCC TCT AGG CTC ATT TAG C TTA TGA AGC AGT GAT GCC AA GTG AGT CAA TTC CCC AAG GTT GTA TTA GTC AAT GTT CTC C GAG ACG GTA GGA AAA GGA G AGC CAA GTT CGA GCC ACT G GTC CCC ATA TTG ATA AAC TAT T ATG AAT AGG GGA TAT GCT GG TTG CAG GGA AAC CAC AGT T TCC TTG GAA TAA ATT CCC GG CGG AGG TTG CAG TGA GTT G GGG AAG GCT ATG GAG GAG A ATG ATG AAT GCA TAG ATG GAT G AAT GTG TGT CCT TCC AGG C
D18S382	UT600	L16292	18pter-18pter	
D18S386	UT754	L18400	18q22.1-18q22.2	
D18S390	UT1227	L15542	18q22.3-18q23	
D18S391	UT1302	L16384	18pter-18p11.22	
D18S814	UT1248	L17776	18pter-18pter	
D18S815	UT1438	L17819	18pter-18qter	
D18S819	UT7251	L30411	18pter-18qter	
D18S851	SHGC 4561	G08002	18pter-18qter	
D21S11	VS17T3	M84567	21q21-21q21	
D21S1240	UT656	L18360	21pter-21qter	
D21S1244	UT761	L16331	21q21-21q22.1	
D21S1413	UT7582	L30513	21pter-21pter	
D21S1412	UT6930	L29680	21pter-21pter	
D21S1411	UT1355	L17803	21pter-21pter	

PENTA E	PAUL1	AC027004 21q	CCC TGG GCT CTG TAA AGA ATA GTG
AMEL		M55418	ATC AGA GCT TAA ACT GGG AAG CTG
HUMTHO		D00269 11p15-15.5	GCT TCC GAG TGC AGG TCA CA
		M68651 2p23-2pter	CAG CTG CCC TAG TCA GCA C
TPOX		M25858 12p12-pter	CAC TAG CAC CCA GAA CCG TC
VWA		11449919 3p	CCT TGT CAG CGT TTA TTT GCC
D3S1358		G08446 5q21-q31	CCC TAG TGG ATG ATA AGA ATA ATC AGT ATG
D5S818		G08616 7q	GGA CAG ATG ATA AAT ACA TAG GAT GGA TGG
D7S820		X14720 5q33.3-34	ACT GCA GTC CAA TCT GGG T
CSF1PO	U63963	M64982 4q28	ATG AAA TCA ACA GAG GCT TG
FGA		G09017 13q22-q31	GGG TGA TTT TCC TCT TTG GT
D13S317			TGA TTC CAA TCA TAG CCA CA
DYS14			TGT CAT AGT TTA GAA CGA ACT AAC G
D13S622	990		CTG AGG TAT CAA AAA CTC AGA GG
D13S304	937		AAC CTG AGT CTG CCA AGG ACT AGC
D13S247	991		TTC CAC ACA CCA CTG GCC ATC TTC
D13S621	642		GCC CCA TAG GTT TTG AAC TCA
D13S250	1250		TGA TTT GTC TGT AAT TGC CAG C
D13S633	7708		ACA GAA GTC TGG GAT GTG GA
D13S243	558		GCC CAA AAA GAC AGA CAG AA
D13S625	1587		CTT TCC ACA GCC ACA TTT GTC
			X CAT CCA GAG CGT CCC TGG CTT

D13S246	740
D13S252	1352
D13S629	6870
D13S624	5236
D13S305	5177
D13S240	472
D13S249	1222
D13S257	2119
D13S256	2120
D13S626	5570
D13S242	557
D13S634	7875
D13S258	2413
D13S303	936
D13S921	2347
D13S251	1329
D13S628	6073
D13S253	1378
D13S627	5821
D13S631	7403
D13S254	1585
D13S248	1213
D18S999	7873
D18S820	7913
D18S818	7162
D18S391	1302
D18S378	485
D18S819	7251
D18S816	5780
D18S814	1248



D18S386	754				
D18S382	600				
D18S817	6365				
D18S815	1438				
D18S390	1227				
D18S812	5025				
D18S380	576				
D18S821	7934				
D21S1418	976				
D21S1411	1355				
D21S1241	657				
D21S1443	CHLC.GATA26A04				
D21S1240	656				
D21S1409	1305				
D21S1250	1332				
D21S1244	761				
D21S1249	1025				
D21S1245	762				
D21S1413	7582				
D21S1408	5040				
D21S1246	973				
D21S1412	6930				
DYS290	708				
DYS391	CHLC.GATA32C10				
D13S241	UT556	L17673	13pter		CCA GGC ACT TTG GGA GGC TG
					ACC CAC TGT ATC CTG GGC A
PD1		AP001752	21q		TGG AAG GTC GAA GCT GAA GTG A
					CCT GTG GCG TGT CTT TTT ACT TTC T
PE1		AC027004	15q		ATC ACT TGA ACC CAG GAG GTG GA
					GGG GAG GCT GTG TAA GAA GTG TT

D8S1179e	G08710	8q24	TTT GGC CAG AAA CCT CTG TAG CC AAC TGA AAC CCT GTG CAT TGT TGT TG TCC AAC CTG AGT CTG CCA AGG A CTT CCA CAC ACC ACT GGC CAT CTT ACA AGG GTG ATT TTC CTC TTT GGT ATC CCA AGT GAT TCC AAT CAT AGC CAC A TGT CAT AGT TTA GAA CGA ACT AAC GAT AG AAA TCT GAG GTA TCA AAA ACT CAG AGG AAT ATG TGA GTC AAT TCC CCA AGT GAA T TGT ATT AGT CAA TGT TCT CCA GAG ACA TGC CCC ATA GGT TTT GAA CTC ACA GAG TGA TTT GTC TGT AAT TGC CAG C CAC TAG CAC CCA GAA CCG TCG TGT CCT TGT CAG CGT TTA TTT GCC GTG GGC TGA AAA GCT CCC GAT GTG ATT CCC ATT GGC CTG TTC CTC TGA GCC ATG TTC ATG CCA CTG ACA AAC CCG ACT ACC AGC AAC TT ACT GCA GTC CAA TCT GGG TGA CAG ATG AAA TCA ACA GAG GCT TGC ATG TAT C GAA GTG CTC GGC ATT GTT AGG AT AGA TCC ATT TGC AGA CTG CCT TAT AAG TGC TCG GCA TTG TTA GGA TT CTA AGC AGA TCC ATT TGC AGA CT CTT CCT ACC ACT GAA CAT AAA CTG CTT AA CAG TGA GCC AAG GTC GTG CCA ACC TGC CAA ATT TTA CCA GGA GGA GAC AGA GAG AGG GAA TAA ACC AAT AAG A GGC AAC AAG AGC AAA ACT CTG C
CSF1POe	X14720	5q33	
D5S818e	G08446	5q21	
D7S820e	G08616	7q	
D21S11e	M84567	21p11.1	
FGAe	M64982	4q28	
TPOXe	M68651	2p23	
THOe	D00269	11p15	
D18S51e	AP001534	18q21.3	
D3S1358e	11449919	3p21	
BKMDY1		Y	
BKMDY2		Y	
D13S317e	G09017	13q22-q31	
D13S258e	L18095	13q21.2-13q31	
D13S631e	L18392	13q31-13q32	
	UT2413		
	UT7403		

D18S391e	UT1302	L16384	18pter-18p11.22	TGG AAA AAT AAT TTC TGG GGG TGG GA CTG GTT TTC GTC TTG AGA AGT CAT G CAC TAT TCC CAT CTG AGT CAC TCA G ACA CAC ACA AAC ATC TCT TTC TAT CTA TAT A GCC TTT ATG AAG CAG TGA TGC CAA ATG ATG AAT GCA TAG ATG GAT GGA TG AAT GTG TGT CCT TCC AGG CTT TCT CGG AGG TTG CAG TGA GTT GAG GGG AAG GCT ATG GAG GAG A TTG CAG GGA AAC CAC AGT TAT ACA TTC TCC TTG GAA TAA ATT CCC GGA AGT TTT CAT CCA GAG CGT CCC TGG C GCT TTC CAC AGC CAC ATT GGT CC CCA GGC ACT TTG GGA GGC TG ACC CAC TGT ATC CTG GGC A TGG AAG GTC GAA GCT GAA GTG A CCT GTG GCG TGT CTT TTT ACT TTC T ATC ACT TGA ACC CAG GAG GTG GA GGG GAG GCT GTG TAA GAA GTG TT TTT GGC CAG AAA CCT CTG TAG CC AAC TGA AAC CCT GTG CAT TGT TGT TG TCC AAC CTG AGT CTG CCA AGG A CTT CCA CAC ACC ACT GGC CAT CTT ACA AGG GTG ATT TTC CTC TTT GGT ATC CCA AGT GAT TCC AAT CAT AGC CAC A TGT CAT AGT TTA GAA CGA ACT AAC GAT AG AAA TCT GAG GTA TCA AAA ACT CAG AGG AAT ATG TGA GTC AAT TCC CCA AGT GAA T TGT ATT AGT CAA TGT TCT CCA GAG ACA
D18S851e	SHGC 4561	G08002	18pter-18qter	
D21S1411e	UT1355	L17803	21pter-21pter	
D21S1412e	UT6930	L29680	21pter-21pter	
D21S1413e	UT7582	L30513	21pter-21pter	
DYS14e	See TSPY			
D13S241	UT556	L17673	13pter	
PD1		AP001752	21q	
PE1		AC027004	15q	
D8S1179e		G08710	8q24	
CSF1POe		X14720	5q33	
D5S818e		G08446	5q21	
D7S820e		G08616	7q	
D21S11e		M84567	21p11.1	

FGAe	M64982	4q28	TGC CCC ATA GGT TTT GAA CTC ACA GAG TGA TTT GTC TGT AAT TGC CAG C CAC TAG CAC CCA GAA CCG TCG TGT CCT TGT CAG CGT TTA TTT GCC GTG GGC TGA AAA GCT CCC GAT GTG ATT CCC ATT GGC CTG TTC CTC TGA GCC ATG TTC ATG CCA CTG ACA AAC CCG ACT ACC AGC AAC TT ACT GCA GTC CAA TCT GGG TGA CAG ATG AAA TCA ACA GAG GCT TGC ATG TAT C GAA GTG CTC GGC ATT GTT AGG AT AGA TCC ATT TGC AGA CTG CCT TAT AAG TGC TCG GCA TTG TTA GGA TT CTA AGC AGA TCC ATT TGC AGA CT CTT CCT ACC ACT GAA CAT AAA CTG CTT AA CAG TGA GCC AAG GTC GTG CCA ACC TGC CAA ATT TTA CCA GGA GGA GAC AGA GAG AGG GAA TAA ACC AAT AAG A GGC AAC AAG AGC AAA ACT CTG C TGG AAA AAT AAT TTC TGG GGG TGG GA CTG GTT TTC GTC TTG AGA AGT CAT G CAC TAT TCC CAT CTG AGT CAC TCA G ACA CAC ACA AAC ATC TCT TTC TAT CTA TAT A GCC TTT ATG AAG CAG TGA TGC CAA ATG ATG AAT GCA TAG ATG GAT GGA TG AAT GTG TGT CCT TCC AGG CTT TCT CGG AGG TTG CAG TGA GTT GAG GGG AAG GCT ATG GAG GAG A TTG CAG GGA AAC CAC AGT TAT ACA TTC
TPOXe	M68651	2p23	
THOe	D00269	11p15	
D18S51e	AP001534	18q21.3	
D3S1358e	11449919	3p21	
BKMDY1		Y	
BKMDY2		Y	
D13S317e	G09017	13q22-q31	
D13S258e	L18095	13q21.2-13q31	
D13S631e	L18392	13q31-13q32	
D18S391e	L16384	18pter-18p11.22	
D18S851e	G08002	18pter-18qter	
D21S1411e	L17803	21pter-21pter	
D21S1412e	L29680	21pter-21pter	
D21S1413e	L30513	21pter-21pter	
	UT2413		
	UT7403		
	UT1302		
	SHGC 4561		
	UT1355		
	UT6930		
	UT7582		

TCC TTG GAA TAA ATT CCC GGA AGT TTT  
CAT CCA GAG CGT CCC TGG C  
GCT TTC CAC AGC CAC ATT GGT CC

DYS14e

See TSPY

7.1.2 TABLE 2 Example of Markers used for genetic analysis embodiment

Primer set	Fluorescent Dye	pmoles
Amelogenin	FAM	Variable from 1-40
DYS14	FAM	Variable from 1-40
D21S11	FAM or TET	Variable from 1-40
D13S631	HEX	Variable from 1-40
D13S258	HEX	Variable from 1-40
D18S51	FAM	Variable from 1-40
D18S851	FAM	Variable from 1-40
D18S391	HEX	Variable from 1-40
D13S317	TET	Variable from 1-40
D21S1413	HEX	Variable from 1-40
D21S1412	TET	Variable from 1-40
D21S1411	FAM	Variable from 1-40

7.1.3 TABLE 3 Example of Markers used for DNA fingerprinting embodiment

Primer set	Fluorescent Dye	pmoles
Amelogenin	FAM	Variable from 1-40
HUMTHO	FAM	Variable from 1-40
D21S11	FAM	Variable from 1-40
D18S51	FAM	Variable from 1-40
VWA	HEX	Variable from 1-40
FGA	HEX	Variable from 1-40
D3S1358	FAM	Variable from 1-40
D5S818	TET	Variable from 1-40
D7S820	TET	Variable from 1-40
CSF1PO	HEX	Variable from 1-40
TPOX	TET	Variable from 1-40

7.1.4 TABLE 4 Comparison of analysis methods

	Fluorescent PCR	FISH	Conventional PCR	PRINS
High reliability	97%	86%	84% for CF	91%
High accuracy	97-99% 97% for (Carrier) in CF	>95%	79% (Unaffected) & 66% (Carrier) for CF	25%
Rapid diagnosis	6 hrs	~4 hrs	8-10 hrs	6 hrs
Diagnosis of sex	Yes	Yes	Possible but poor reliability & accuracy	Yes
Diagnosis of single-gene defects	Yes	No	Yes	No
Diagnosis of trisomies	Yes	Yes	No	Yes
Confirmation of diagnosis	Yes	No	No	No
DNA fingerprinting	Yes, high specificity 1 in 100 million.	No	Limited ~1 in 10	No
Detection of contamination	Yes	No	Very limited	No
Simultaneous diagnoses	Sex, CF, trisomies & DNA fingerprint	Trisomies	No	No
No of chromosomes simultaneously analysed	~26	3-5	1	3



